

1 AGCATCCTGA GTAATGAGTG GCCTGGGCGG GAGCAGGCGA GGTGGCCCGA GCCGTGTGGA CCAGGAGGAG CGCTTTCCAC AGGGCCTGTG GAGGGGGGTG
TCGTAGGACT CATTACTCAG CGGACCGCGC CTCGTCCGCT CCACCGGCCT CGGCACACCT GGTCTCTCTC GCGARAGGTG TCCCGGACAC CTGCCCCACAC
1 M S G L G R S R R G G R S R V D Q E E R F P Q G L W T G V
101 GCTATGAGAT CCTGCCCCGA AGAGCACTAC TGGGATCCTC TGTGGGTAC CTGCATGTCC TGCARACCA TTGCRACCA TCAGAGCCAG CGCACCTGTG
CGATACTCTA GGRCGGGGT TCTCGTCATG ACCCTAGGAG ACGACCCATG GACGTACAGG ACGTTTGGT AAAGTTGGT AGTCTGGTC GCGTGGACAC
30 A M R S C P E E Q Y W D P L L G T C M S C K T I C N H Q S Q R T C A
201 CAGCCTTCTG CAGGTCACTC AGCTGCCCGA AGGAGCAAGG CRAATTCTAT GACCATCTCC TGGGGACTG CATCAGCTGT GCCTCCATCT GTGCACAGCA
GTCCGAGAC GTCCAGTACG TCGACGGGT TCTCGTTTCC GTTCAAGATA CTGTAGAGG ACTCCCTGAC GTAGTCGACA CGGAGGTAGA CACTGTCTCT
64 A F C R S L S C R K E Q G K F Y D H L L R O C I S C A S I C G Q H
301 CCCTAGACAA TGTGATRACT TCTGTAGAA CRACTCAGG AGCCAGTGA ACCTTCCACC AGAGCTCAGG AGACAGCCGA GTGAGNAGT TGAACACAT
GGGATTCGTT ACACGTATGA AGACACTCTT GTTCGAGTCC TCGGTCCTT TCGAGTTCG TTGAGTCCA GAGGGCCCG ACTTCGACTC ACCTCTTCA ACTTTGTGA
97 P K Q C A Y F C E N K L R S P V N L P P E L R R Q R S G E V E N N
401 TCAGACAACT CGGGRAGTA CCAAGGATTG GAGCACAGG GCTCAGAAGC AGTCCAGCT CTCCCGGGG TGAAGCTGAG TGCAGATCAG GTGSCCCTGG
AGTCTGTGA GCCCTTCCAT GGTTCCTAAC CTGTGCTC CGAGTCTTCG TTGAGTCCA GAGGGCCCG ACTTCGACTC ACCTCTAGTC CACCGGAC
130 S D N S G R Y Q G L E H R G S E A S P A L P G L K L S A D Q V A L V
501 TCTACAGCAC GCTGGGGCTC TGCCTGTGTG CCGTCTCTG CTGCTTCTG GTGGCGTGG CTTGCTTCTT CAGAGAGG GGGGATCCCT GCTCTGCCA
AGATGTCTG CGACCCCGAG ACGACACAC CCGAGGAGAC GAGCAGGAC CACCGCCACC GGACGAGGA GTTCTTCTCC CCCTAGGA CGAGACGGT
164 Y S T L G L C L C A V L C C F L V A V A C F L K K R G D P C S C Q
601 GCCCGCTCA AGCCCCGTC AAGTCCGGC CAGTCTTCC CAGGATCAG CGATGAAGC CGGCAGCCCT GTGAGCACAT CCCCGAGCC AGTGAGACC
CGGGCGGAGT TCGGGGGCAG TTTCAGGCGG GTTCAGAAGG GTCCTAGTC GCTACCTTCG GCGTCCGGA CATCTGTGA GGGGCTCGG TCACCTCTGG
197 P R S R P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T
701 TGCAGCTTCT GCTTCCCTGA GTGCAGGGG CCGAGGCGAG AGAGCCAGT CACGCTGGG ACCCCCGACC CCACTTGTG TGAAGGTGG GGGTCCACA
ACGTGAGGA CAGAGGAGT CAGTCCCGC GGTGCGTCC TCTGCGTCA GTGCGGACCC TGGGGGTGG GGTGAACAGG ACCTTCCACC CCCAGGTGT
230 C S F C F P E C R A P T Q E S A V T P G T P D P T C A G R W G C H T
801 CCAGGACCAAC AGTCTCTGAG CCTGSCCAG ACATCCCAAG CAGTGGCCTT GGCATTGTGT GTGTGCCCTG CCGAGAGGGG GGCCAGGTG CATTAATGGG
GGTCTCTGTG TCAGGACGTC GAGAGGGGTG TGTAGGCTCT GTCACCGAA CCGTACACA CACAGGAGG GGTCTCTCCC CCGGTCCAC GTATTACCC
264 R T T V L Q P C P H I P D S G L G I V C V P A Q E G G P G A O

FIG. 1A

901 GGTGAGGAG GGAAGGAGG AGGAGAGAG ATGGAGAGGA GGGAGAGAGG AAGAGAGAGT GGGAGAGAGG GAGAGAGATA TGAGAGAGA GAGCAGAGG
 CCAGTCCCTC CATTCCCTC TCCCTCTCTC TACCTCTCTC CCCCTCTCTC TTCTCTCTCA CCCCTCTCCC CTCTCTCTAT ACTCTCTCT CTCTCTCTCC
 1001 AGGCAGNAAG GGAGAGNAAC AGGAGAGACA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA
 TCCGTCTTC CCTCTCTTG TCTCTCTGT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CCCTCTCTCT CTCTCTCTCT TTCTCTCTCT CTCTCTCTCT CTCTCTCTCT
 1101 AGGAGAGAGA CAGGAGAGAGA AGGAGAGAGG CAGAGAGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA GAGAGGAGGA
 TCCCTCTCTCT GTCCGTCTCT TCCCTCTCTCC GTCTCTCTCT CTCTCTCTCT CTCTCTCTCT CCCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT
 1201 GAGCAGGAGG TCGGGGCACT CTGAGTCCCA GTTCCCACTG CAGCTGTAGG TCGTCATCAC CTACCCACAC GTGCAATAAA GTCTCTCTCT GTCTCTCTCA
 CTCGTCTCTC AGCCCGGTGA GACTCAGGT CAGGGTCAC GTCCACATCC AGCAGTAGTG GATTGGTGTG CACGTATATT CAGGAGCAGG GACGACGAGT
 1301 CAGCCCCGA GAGCCCTCC TCCGAGAGAA TAAACCTTT GGCAGCTGCC CTCTCTCAAA AAAAAAAAAA AAAAAA
 GTCGGGGCT CTCGGGAGG AGGACCTCTT ATTTGGAA CCGTCGACGG GAAGAGTTT TTTTCTTT TTTTCTTT

FIG. 1B

HTACI(255)	10	20	30	40	50
HTACI	M S C L C R S R R G G R S R V Q Q E E R F P Q G L W T G V A M R S C P E E Q Y W D P L L G T C M S C				
	60	70	80	90	100
	M S G L C R S R R G G R S R V Q Q E E R F P Q G L W T G V A M R S C P E E Q Y W D P L L G T C M S C				
HTACI(265)	110	120	130	140	150
HTACI	K T I C N H Q S Q R T C A A F C R S L S C R K E Q G K F Y D H L L R D C I S C A S I C G Q H P K Q C				
	160	170	180	190	200
	K T I C N H Q S Q R T C A A F C R S L S C R K E Q G K F Y D H L L R D C I S C A S I C G Q H P K Q C				
HTACI(265)	210	220	230	240	250
HTACI	A Y F C E N K L R S P V N L P P E L R R Q R S G E V E N N S D N S G R Y Q G L E H R G S E A S P A L				
	260	270	280	290	300
	A Y F C E N K L R S P V N L P P E L R R Q R S G E V E N N S D N S G R Y Q G L E H R G S E A S P A L				
HTACI(265)	310	320	330	340	350
HTACI	P G L K L S A D Q V A L V Y S T L G L C L C A V L C C F L V A V A C F L K K R G D P C S C Q P R S R				
	360	370	380	390	400
	P G L K L S A D Q V A L V Y S T L G L C L C A V L C C F L V A V A C F L K K R G D P C S C Q P R S R				
HTACI(265)	410	420	430	440	450
HTACI	P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T C S F C F P E C R A P T Q E S A V T P G T				
	460	470	480	490	500
	P R Q S P A K S S Q D H A M E A G S P V S T S P E P V E T C S F C F P E C R A P T Q E S A V T P G T				
HTACI(265)	510	520	530	540	550
HTACI	P D P T C A G R T A P P R E G Z				
	560	570	580	590	600
	P D P T C A G R T A P P R E G Z				

FIG. 1C

1 ARAGACTCAA CTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG ACACAGACAG CCCCCTAAG ACCCAGAA GCAGGGGAAG
TTCTGAGTTT GAATCTTTGA ACTTAATCTA CACCATAGT TTAGGAATGC ACGGCGCTTC TGTGCTGTC GGGGCAATTC TTGGGTGCTT CGTCCGCTTC
101 TTCATTGTC TCACATTCT AGCTGCTCTT GCTGCATTG CTCTGGAATT CTGTGAGAGA TATTACTTGT CCTTCAGGC TGTCTTTCT GTAGCTCCCT
AAGTAACAG AGTTGTAAGA TCGACGAGAA CGACGTAAAC GAGACCTTAA GACATCTCT ATAATGARCA GGAAGTCCG ACAGAAAGA CATCGAGGA
201 TGTTCCTTT TTGTGATCAT GTTCAGATG GCTGGGAGT GCTCCCAAAA TGAATATTT GACAGTTTGT TGCATGCTTG CATACCTGT CAACCTCGAT
ACAAAAGAAA AACACTAGTA CAACGCTAC CGACCCGTCA CGAGGGTTTT ACTTATAAAA CTGTCAAACA ACGTACGAAC GTATGGAACA GTTGAAGCTA
1 Me tLeuGlnMet AlaGlyGlnC ysSerGlnAs nGluTyrPhe AspSerLeuL euHisAlaCy sileProCys GlnL uArgC
301 GTTCTTCTAA TACTCTCTCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAAT GTGAGAAAGG AACGAATGCG ATTCTCTGA CCTGTTTGGG
CAAGAGATT ATGAGGAGGA GATTGTACAG TCGCAATAAC ATTACGTTCA CACTGGTTAA GTCACCTTCC TTAGAGACCT TGAACAAACC
29 ysSerSerAs nThrProPro LeuThrCysG lnArgTyrCy sAsnAlaSer valThrAsnS erValLysG l yThrAsnAla lleLeuTyrP hrCysLeuG l
401 ACTGAGCTTA ATAATTTCTT TGSCAGTTT CGTGCTAATG TTTTGTCTAA GGAAGATAAG CTCTGAAACA TTTAAAGGAGG AGTTTAAAA CACAGGATCA
TGACTCGAAT TATTAAAGAA ACCGTCAAAA GCACGATTAC AAAAAGGATT CCTTCTATT CAGACTTGGT AATTTCTGC TCAATTTTT GTGCTCTAGT
62 yLeuSerLeu lleIleSerL euAlaValPh eValLeuMet PheLeuLeuA rgLysIleSe rSerGluPro LeuLysAspG luPheLysAs nThrGlySer
501 GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAGAGCA GGACTGGTGA TGAAATTTAT CTTCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT
CCAGAGGACC CGTACCGATT GTAACCTGGAC CTTTCTCTCGT CCTGACCACT ACTTTAATAA GAAGGCTCTC CGGAGCTCAT GTGCCACCTT CTACGTTGA
95 GlyLeuLeuG lyMetalaAs nIleAspLeu GluLysSerA rgThrGlyAs pGluIlelle LeuProArgG lyLeuGluTy rThrValGlu GluCysThrC
601 GTGAAGACTG CATCAAGAGC AAACCGAAG TCGACTCTGA CCATTGCTTT CCACTCCCAG CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC
CACTTCTGAC GTAGTTCTCG TTTGGCTTCC AGCTGAGACT GGTAAACGAA GGTGAGGGTC GATACCTCCT TCCGCGTTGG TAAGAACAGT .GGTCTTTTG
129 ysGluAspCy sileLysSer LysProLysV alAspSerAs pHisCysPhe ProLeuProA laMetGluG l uGlyAlaThr lleLeuValT hrThrLysTh
701 GAATGACTAT TGCAAGAGCC TGCCAGCTGC TTTGAGTGTCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAAACA TTTCGACTCG AGCAGTGCCA
CTTACTGATA ACGTCTCGG ACGGTGACG AAACCTCACGA TGCCTCTATC TCTTTAGTTA AAGACGATCC ATTAATTGGT AAAGCTGAGC TCGTCACGGT
162 rAsnAspTy r CysLysSerL euProAlaAl aLeuSerAla ThrGluIleG l uLysSerIl eSerAlaArg OC+
801 CTTTAAAAAT CTTTGTCTAG ATAGATGAT GTGTCAGATC TCTTTAGGAT GACTGTATTT TTCACTTGGC GATACAGCTT TTGTCTCTCT AACTGTGGAA
GAATTTTGA GAACACAGTC TTATCTACTA CACAGTCTAG AGAAATCCTA CTGACATARA AAGTCAACGG CTATGTGCGA AAACAGGAGA TTGACACCTT
901 ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAACTTC CTGTTTCA TGATTAAGT CTTTTTTTTT CCTGA
TGAGAAATAC AATCTATATA AAGAGATCCA ATGACAACCC TCGAATTACC ATCTTTGAAG GAACCAAGT ACTAATTTCA GAAAAAATAA GGACT

FIG. 2

1 ATGGATGACT CCACAGAAAG GGAGCAGTCA CGCCTTACTT CTGCGCTTAA GAAAGAGAA GAAATGAAC TGAGGAGTG TGTTCCATC CTCACAGGA
TACCTACTGA GGTGTCTTC CCTCGTCACT GCGGAATGAA GAACGGAAT CTTTCTCTT CTTTACTTG ACTTCTCAC ACAGAGGTAG GAGGTGCTT
1 M D D S T E R E Q S R L T S C L K K R E E M K L K E C V S I L P R K
101 AGGAAAGCCC CTCTGTCCGA TCCTCCNAAG ACGGAAGCT GCTGGCTGCA ACCTTGCTGC TGGCACTGCT GTCTTGCTGC CTCACGGTGG TGCTTTCTTA
TCTTTGCGG GAGACAGCT AGGAGGTTTC TGCTTTTCA CGACCGACGT TGGACGACG ACOGTGACGA CAGAACGACG GAGTGCCACC ACAGAAAGAT
35 E S P S V R S S K D G K L L A A T L L L A L L S C C L T V V S F Y
201 CCAGGTGGCC GCCTGCAAG GGGACCTGCC CAGCTCCGG GCAGAGCTGC AGGCCACCA CGCGAGAA GCGCAGCAG GAGCAGGAGC CCCAAGGCC
GGTCCACCG GCGGACGTTT CCTGGACCG GTCCGAGCC CGTCTGACG TCCCGTGGT GCGCTCTTC GACGGTCTC CTCGTCTCG GGGTTCGGG
68 Q V A A L Q G D L A S L R A E L Q G H A E K L P A G A G A P K A
301 GGCTTGAGG AAGTCCAGC TGTACCGCG GACTGAAA TCTTGNACC ACCAGCTCA GGAGAGGCA ACTCCAGTCA GAACAGCA AATAAGCGTG
CCGACCTCC TTGAGGTG ACAGTGGCG CCTGACTTT AGAACTTGG TGGTCGAGT CCTCTCGT TGAGTCACT CTTGTCTCT TTATTGCRAC
101 G L E E A P A V T A G L K I F E P P A P G E G N S S Q N S R N K R A
401 CCGTTCGGG TCCAGAGAA ACAGTCACTC AAGCTGCTT GCACTGATT GCAGACAGT GAACACCAAC TATACAAA GGATCTTACA CATTTGTTCC
GGCAAGTCCC AGTCTCTTT TGTCACTGAG TTCTGACGAA CGTCTACTAA CGTCTGCTAC TTGTGGTGG ATATGTTTTT CCTAGATGT GTAAACAAGG
135 V Q G P E E T V T Q D C L Q L I A D S E T P T I Q K G S Y T F V P
501 ATGCTTCTC AGCTTTTAAA GGGGAAGTGC CCTAGAGAA AAGAGANTA AATATTGGT CAAAGAACT GGTACTTTT TTATATATGG TCAGTTTAA
TACGAGAGG TCGAATTTT CCCCTTCACG GGATCTTCTT TTTCTCTTAT TTTATACCA GTTTCTTTGA CCAATGAATA AATATATACC AGTCCAAAT
168 W L L S F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L
601 TATACTGATA AGACTACGC CATGGGACAT CTATTCAGA GGAAGAGGT CCAATGCTTT GGGATGAAT TGAGTCTGGT GACTTGTGT CGATGTATTC
ATATGACTAT TCTGGATGCG GTACCTGTA GATTAAGTCT CCTTCTTCCA GTTACAGAA CCCCTACTTA ACTCAGACCA CTGAACAA GCTACATAG
201 Y T D K T Y A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q
701 AATATAGCC TGAACACTA CCAATATTT CCTGCTATTC AGCTGGCATT GCMAACTGG AAGAGGAGA TGAATCCAA CTTCATATAC CAAGAAATA
TTTATACCG ACTTGTGAT GGGTATTAA GGAAGATAG TCGACCGTAA CGTTTGACC TTCTTCTCT ACTTGAGTT GAACGTATG GTTCTCTTT
235 N M P E T L P N N S C Y S A G I A K L E E G D E L Q L A I P R E N
801 TGCACATA TCACTGGATG GAGTGTAC ATTTTGGT GCATGAAC TGCTGTA
ACGTGTTTAT AGTGACCTAC CTCTACAGTG TAAACCA CGTAACTTTG ACACACT
268 A Q I S L D G D V T F F G A L K L L O

FIG. 3

1 GGTACGAGGC TTCTTAGAGG GACTGGAACC TAATTTCTCT GAGGCTGAGG GAGGCTGAGG GGTCTCAGAG CACGCTGGC CCACGACGG AGTCCACAGG
CCATGCTCCG AAGGATCTCC CTGACCTTGG ATTAAGAGGA CTCGACCTCC CTCCCACCTC CCAGAGTTCC GTTGGACCG GGTGCTGCC TCACGGTCTCT

101 GCACTAACAG TACCCTTAGC TTGCTTTCTT CCTCCCTCCT TTATTTCTTC AGTTCTCTTT TTATTTCTCC TTGGTAACA ACCTTCTTCC CTTCTGCACC
CGTGATGTC ATGGGAATCG AACGAAGGA GGAGGGAGGA AATATAAAG TTCAAGGAAA AATAAAGAG AACCATTTGT TGGAGAGG GRACACGTGG

201 ACTGCCCGTA CCTTACCCG CCCGCCACC TCCTTGCTAC CCACCTCTTG AAACCAACAGC TGTGGCAGG GTCCACAGT CATGCCAGCC TCATCTCCTT
TGACGGGCAT GGGATGGGC GGGGCGGTGG AGGAACGATG GGTGAGAAC TTGTGTGTGG ACAACCGTCC CAGGGGTGGA GTACGCTCG AGTAGAGGAA
M P A S S P F

301 TCITGCTAGC CCCRAAGG CCTCCAGGCA ACATGGGGG CCCAGTCAAG GAGCCGGCAC TCTCAGTTGC CCTCTGGTTG AGTTGGGGG CAGCTCTGGG
AGNACGATCG GGGGTTTCCG GGAGTCCGT TGTACCCCCC GGTCTAGTCT CTGCGCCGTG AGAGTCAAG GGAGCAAC TCACCCCCC GTCGAGACCC
8 L L A P K G P P G N M G G P V R E P A L S V A L W L S W G A A L G

401 GGCCGTGGCT TGTGCCATGG CTCTGCTGAC CCAACAACA GAGCTGCAGA GCTCAGGAG GCTCAGGAG GAGAGGTGAG CCGTGCAGG GGACAGGAG CCCTCCCCAG
CCGGACCCGA ACACGGTACC GAGACGACTG GGTGTTTGT CTGACGCTCT CGAGTCTCTC TCCTCACTCG CCCGACGTCC CCTGTCTTCC GGGGAGGCTC
41 A V A C A M A L L T Q Q T E L Q S L R R E V S R L Q G T G G P S Q

501 AATGGGAAG GGTATCCCTG GCAGAGTCTC CCGAGGAGA GTTCCGATGC CTEGAGGCC TGGAGATG TGGAGATG GGGAGAGATC CCGGAAGAG AGAGAGTGC
TTACCCCTTC CCATGGGAC GGTCTCAGG GGCCTGCTCT CAGGCTAGG GGACCTTCGG ACCCTCTTAC CCCTCTCTAG GGCCTTTTCC TCTCTCAAG
74 N G E G Y P W Q S L P E Q S S D A L E A W E N G E R S R K R R A V L

601 TCACCCAAA ACAGAGAG CAGCACTCTG TCCTGCACCT GGTCCCATTT AACGCCACCT CCAAGGATGA CTCGATGTG ACAGAGTGA TGTGCAAC
AGTGGGTTT TGTCTTCTC GTCGTGAGAC AGGACGTGGA CCAAGGGTAA TTGGGGTGA GGTCTCTACT GAGGTACAC TGTCTCCACT ACACGTTGG
108 T Q K Q K K Q H S V L H L V P I N A T S K D D S D V T E V M W Q P

701 AGCTCTTAGG CCGTGGAGG GCCTACAGG CCAAGCATAT GGTGTCCGAA TCCAGGATGC TGGAGTTTAT CTGCTGTATA GCCAGTCTCT GTTTCAGAC
TCGRGATCC GCACCCCTCT CCGATGTCCG GGTCTCTATA CCAAGGCTT AGGTCTCTAG ACCTCAATA GACGACATAT CCGTCCAGGA CAAAGTTCTG
141 A L R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L F Q D

801 GTGACTTTCA CCATGGGTCA GTGGTGTCT CAGAGAGGCC AAGGAAGGCA GGAGACTCTA TTCGATGTA TAAGAGATAT GCCCTCCAC CCGGACCGGG
CACTGAAAGT GGTACCCAGT CCACACAGA GCTCTTCCGG TTCTTCCGT CCTCTGAGT AAGGTACAT ATTCTTCATA CCGGAGGTG GGCCTGGCCC
174 V T F T M G Q V V S R E G Q G R Q E T L F R C I R S M P S H P D R A

901 CCTACACAG CTGCTATAGC GCAGGTGTCT TCCATTTTCA CCAAGGGGAT ATTCTGAGTG TCATAATTC CCGGGCAAGG GCGAAGCTTA ACCTCTCTCC
GGATGTTGTC GAGGATATCG CGTCCACAGA AGTAATATGT GGTCCCCCTA TRAGACTCAC AGTATTAAG GGGCCGTTCC CGCTTTGAAT TGGAGAGAG
208 Y N S C Y S A G V F H L H Q G D I L S V I I P R A R A K L N L S P

FIG. 4A

1001 ACATGGAAAC TTCCTGGGGT TTGTGAABACT GTGATTGIGT TATRAAABGT GGCTCCCAGC TTGGAAAGACC AGGGTGGGTA CATACTGGAG ACAGCCAAAGA
 TGTAACCTGG AAGGCCCAAC AACACTTTGA CACTACACACA ATATTTTCA CCGAGGGTGG AACCTTCTGG TCCCACCCAT GTATGACCTC TGTGGTTCT
 241 H G T F L G F V K L Q
 1101 GCTGAGTATA TAAAGGAGAG GGRATGTGCA GGRACAGAGG CATCTTCCTG GGTITGGCTC CCGTTTCCTC ACTTTTCCCT TTTCATTCCC ACCCCCTAGA
 CGACTCATAT ATTTCCTCTC CCTTACACGT CCTGTCTCC GTAGAAGGAC CCAACCCGAG GGGCRAGGAG TGAAABAGGA AAGTAAGGG TGGGGGATCT
 1201 CTTTGATTTT ACGGATATCT TGCTTCTGTT CCGCATGGAG CTCGAAATTC TTGCTGTGT GTAGATGAGG GGGGGGGGAC GGGCCGCCAGG CATTTGTTGAG
 GAACTAABA TGCCTATAGA ACGAAGACHA GGGGTACCTC GAGGCTTARG AACGCACACA CATCTACTCC CCGCCCCCTG CCGCGGGTCC GTAACAGTC
 1301 ACCTGGTGGG GGGCCACTGG AAGCATCCAG AACAGCACCA CCATCTTA
 TGGACCAGCC CCGGGTGACC TTCTAGGTC TTGTCGTGGT GGTAGAT

FIG. 4B

TACIs

agcatcctgagtaATGAGTGGCCTGGGCGGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGG
AGGAGCGCtGGTCACTCAGCTGCCGCAAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGAC
TGCATCAGCTGTGCCCTCCATCTGTGGACAGCACCCCTAAGCAATGTGCATACTTCTGTGAGAACAA
GCTCAGGAGCCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGGAGTGGAGAAGTTGAAAACA
ATTGAGACAACCTCGGGAAGGTACCAAGGATTGGAGCACAGAGGCTCAGAAGCAAGTCCAGCTCTC
CCGGGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGGCTCTGCCTGTG
TGCCGTCTCTGCTGCTTCTTGGTGGCGGTGGCCTGCTTCTCAAGAAGAGGGGGGATCCCTGCT
CCTGCCAGCCCCGCTCAAGGCCCCGTCAAAGTCCGGCCAAGTCTTCCCAGGATCACGCGATGGAA
GCCGGCAGCCCTGTGAGCACATCCCCGAGCCAGTGGAGACCTGCAGCTTCTGCTTCCCTGAGTG
CAGGGCGCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCCGACCCCACTTGTGCTGGAAGGT
GGGGGTGCCACACCAGGACCACAGTCTTGCAGCCTTGCCACACATCCAGACAGTGGCCTTGGC
ATTGTGTGTGTGCCAGGAGGGGGGGCCAGGTGCATAAatgggggtcagggaggggaaagga
ggagggagagagatggagaggaggggagagagaaagagaggtggggagaggggagagagatatga
ggagagagagacagaggaggcagaaaggagagagaaacagaggagacagagagggagagagagaca
gagggagagagagacagaggggaagagaggcagagagggaaagaggcagagaaggaaagagacag
gcagagaaggagagaggcagagagggagagaggcagagagggagagaggcagagagacagagagg
gagagagggacagagagagatagagcaggaggtcggggcactctgagtcccagttcccagtgag
ctgtagggtcgatcacctaaccacacgtgcaataaagtccctcgctgctgctcacagcccc
gagagccccctcctcctggagaataaaacctttggcagctgcccttcctcaaaaaaaaaaaaaaaaa
aaaa

Fig. 5A

TACIs :

MSGLGRSRRGGRSRVDQEERWSLSCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENKLRSP
VNLPPELRRQRSGEVENNSDMSGYQGLEHRGSEASPALFGLKLSADQVALVYSTLGLCLCAVLC
CFLVAVACFLKKRGDFCSCQPRSRPRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAFT
QESAVTPGTPDPTCAGRWGCHTRTTVLQPCPHIPDSGLGIVCVPAQEGGPG

Fig. 5B

human BR3:

cgtcggcaccATGAGGCGAGGGCCCCGGAGCCTGCGGGGCAGGGACGCGCCAGCCCCACGCCCT
GCGTCCCGGCCGAGTGCTTCGACCTGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACG
CCGCGGCCGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAGCCGCAGGAGTC
GGTGGGCGCGGGGGCCGGCGAGGCGGCGCTGCCCCTGCCCGGGCTGCTCTTTGGCGCCCCCGCGC
TGCTGGGCCTGGCACTGGTCCTGGCGCTGGTCCTGGTGGGTCTGGTGAGCTGGAGGCGGCGACAG
CGGCGGCTTCGCGGCGCGTCCTCCGCAGAGGCCCCCGACGGAGACAAGGACGCCCCAGAGCCCCT
GGACAAGGTCATCATTCTGTCTCCGGGAATCTCTGATGCCACAGCTCCTGCCTGGCCTCCTCCTG
GGGAAGACCCAGGAACCAACCCACCTGGCCACAGTGTCCCTGTGCCAGCCACAGAGCTGGGCTCC
ACTGAACTGGTGACCACCAAGACGGCCGGCCCTGAGCAACAATAGcagggagccggcaggaggtg
gccccctgccc

Fig. 6A

BR3:

MRRGPRSLRGRDAPAPTPCVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGA
GAGEAALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRQRRRLRGASSAEAPDGDKDAPEPLDKV
IILSPGISDATAPAWPPPGEDEGTTTPGHSVPVPATELGSTELVTTKTAGPEQQ

Fig. 6B

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 15 = 33.3%

FIG. 7A

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

FIG. 7B

O.D (450 nm)

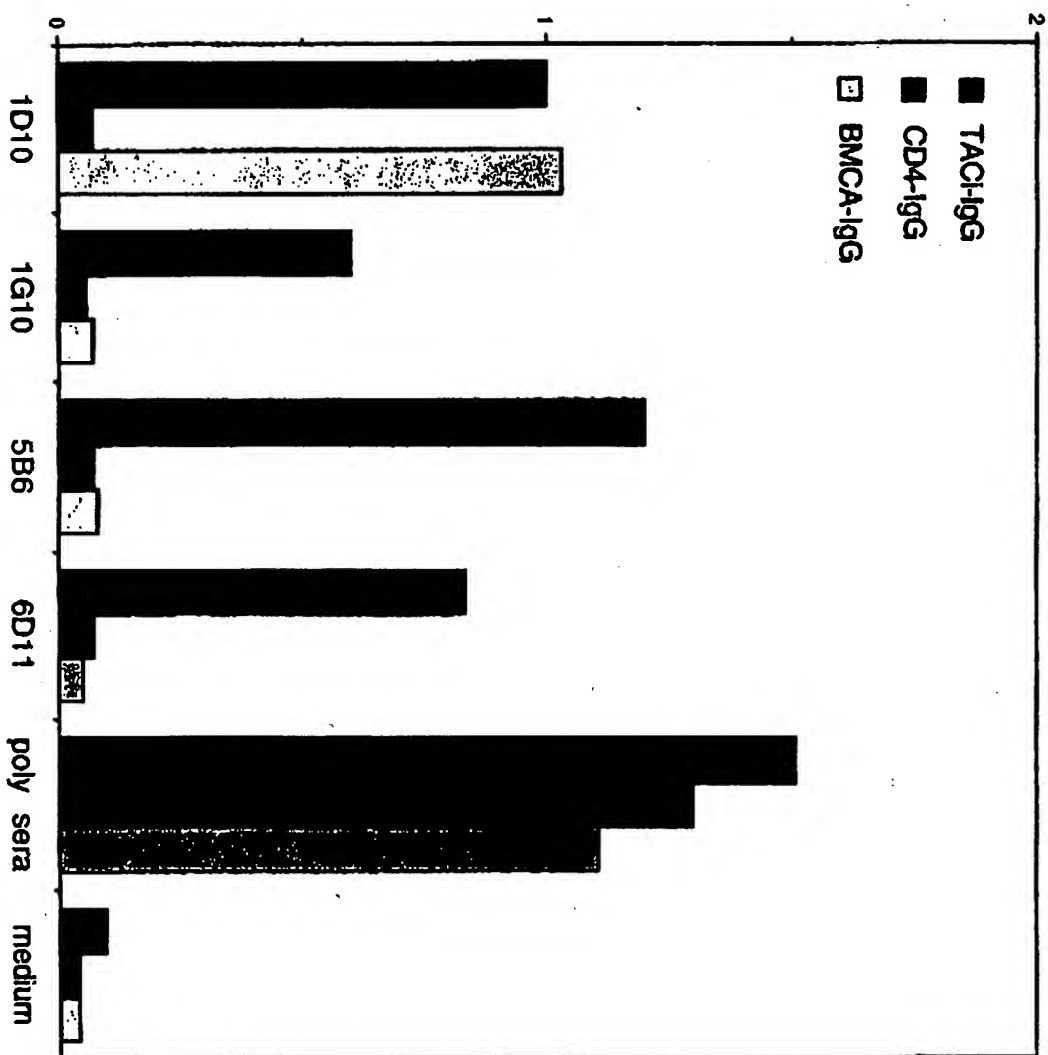


FIG. 8

mAbs (culture Supernatant)

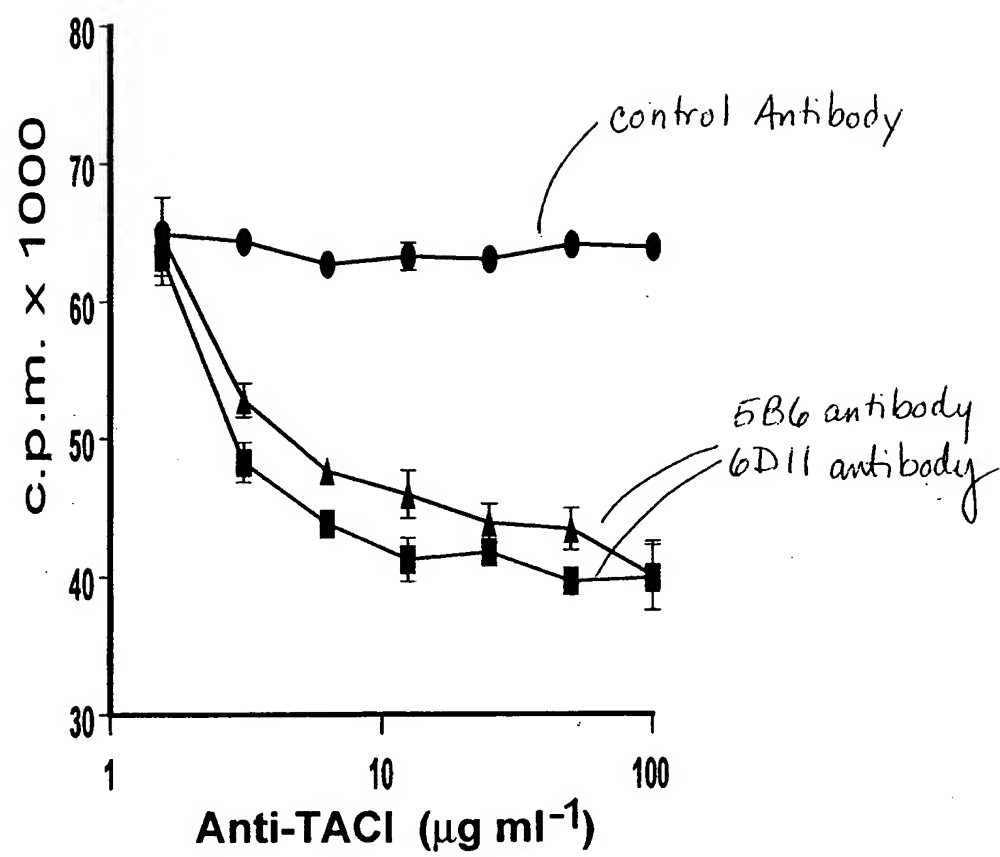


Figure 9

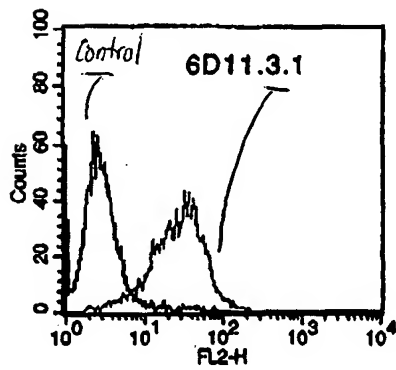
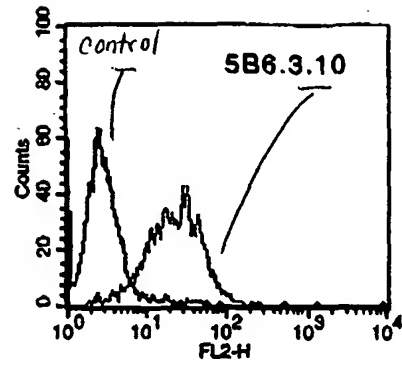
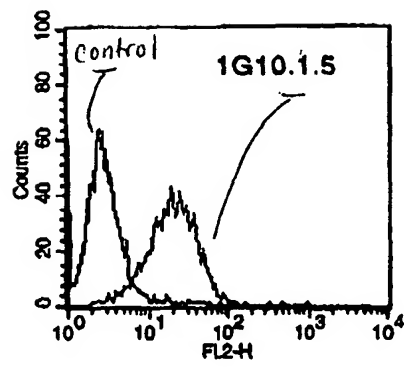


FIG. 10

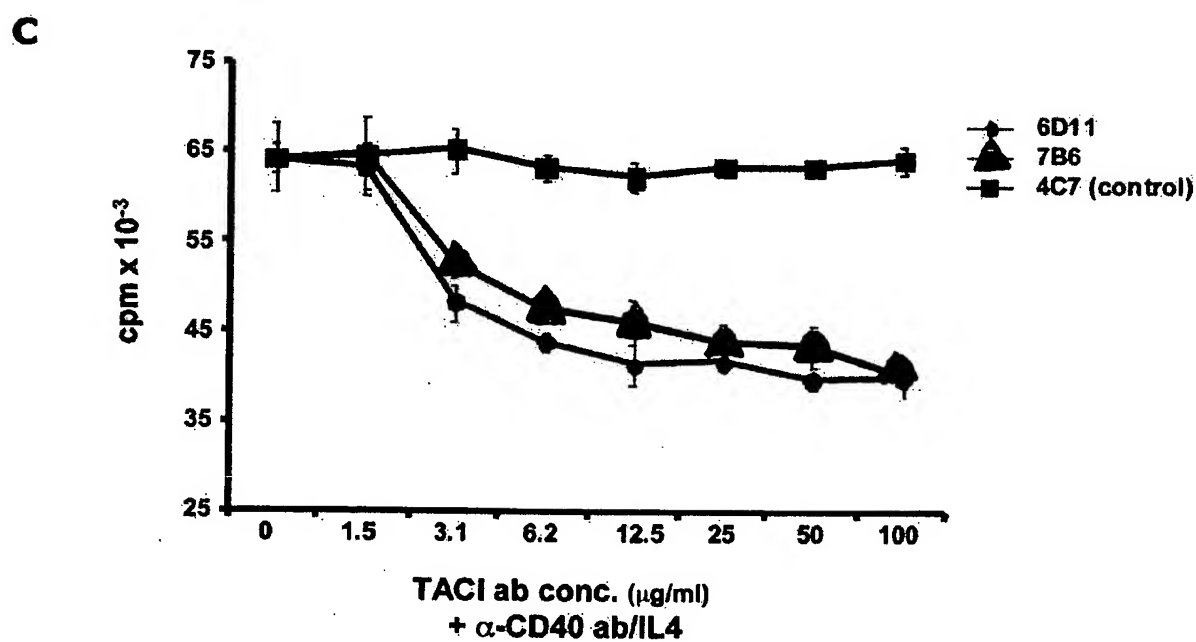
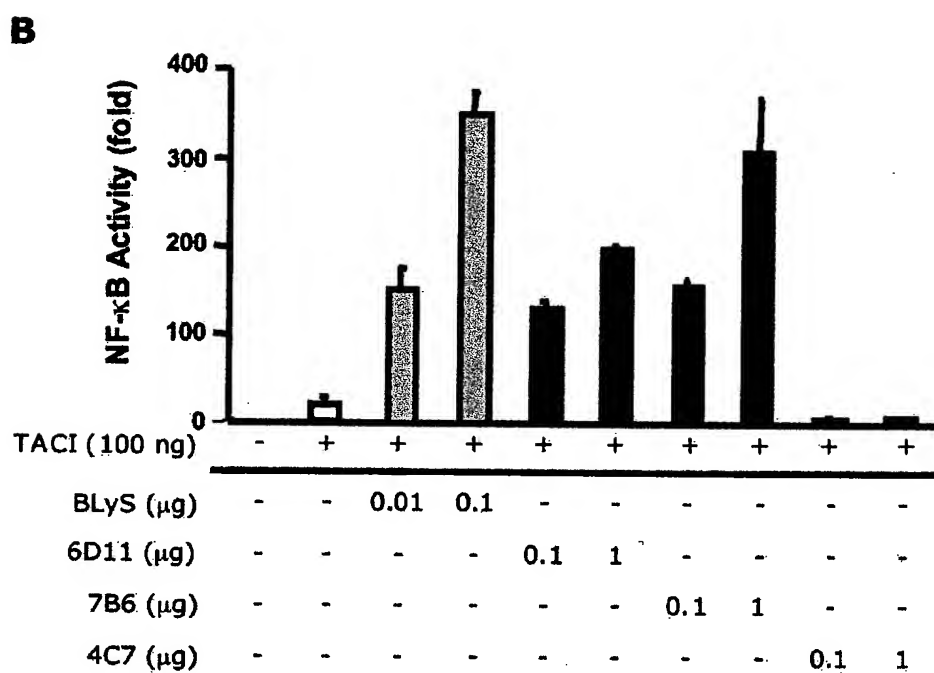
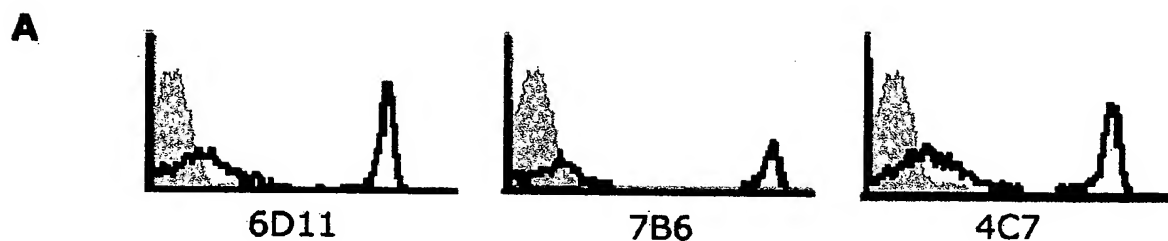


FIG. 11